

ABSTRACT

PROCESS FOR TYPING OF HCV ISOLATES

The invention relates to a process for genotyping any HCV isolate present in a biological sample, previously identified as being HCV positive, and for classifying said isolate according to the percentage of homology with other HCV isolates, comprising the steps of:

- contacting said sample in which the ribonucleotides or deoxyribonucleotides have been made accessible, if need be, under suitable denaturation, with at least one probe from about 10 to about 40 nucleotides, with said probe being liable to hybridize to a region being in the domain extending from nucleotide at position -291 to nucleotide at position -66 of the 5' untranslated region of one of the HCV isolates represented by their cDNA sequences, with said numbering of position beginning with the first ATG codon of the open reading frame encoding the HCV polypotein, or with said probe being complementary to the above-defined probes,

- detecting the complexes possibly formed between said probe and the nucleotide sequence of the HCV isolate to be identified.

(No figure)

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